AMENDMENTS TO THE SPECIFICATION

In the Title, please replace "NEW METHOD" with the following:

METHOD OF SCREENING FOR A MODULATOR OF CARBOXYL ESTER LIPASE BINDING

At page 12 of the specification, please replace the paragraph at lines 13-23 with the following:

Western blot and RT-PCR analysis of CEL in macrophages. ~~Panel A~~Figure 4A shows a Western blot analysis of cell culture media collected from primary monocytes, differentiated into macrophages for up to nine days, at the indicated time points. The "medium" lane represents a control sample of cell culture medium that had not been in contact with the cells. ~~Panel B~~Figure 4B shows cell lysate samples from fully differentiated monocyte-derived macrophages treated with LPS (1 μg/ml), IFN-γ(200 U/ml) or oxLDL (50 μg protein/ml) for 24 hours. The corresponding analysis of CEL mRNA by RT-PCR is shown in ~~panel C~~Figure 4C. Amplification of GAPDH ensured equal amounts of RNA in the samples. The CEL primers were designed to yield a 579 bp product with amplification of cDNA and a 2443 bp product in the case of amplification of contaminating genomic cDNA. The GAPDH primers yield a 597 bp product when amplifying cDNA and 1090 bp when amplifying genomic DNA. No amplification of genomic DNA was observed.

At page 12 of the specification, please replace the paragraph at lines 25-32 with the following:

CEL is abundant in LDL fractions of human serum. ~~Panel A~~Figure 5A shows intense staining for CEL and apoB in the core region of a plaque in an atherosclerotic carotid artery. ~~Panel B~~Figure 5B shows a Western blot with chylomicron-rich serum from two

donors (2 μg protein/lane). While CEL is absent in the chylomicron/VLDL fraction it is abundant in the HDL/LDL fraction. ~~Panel C~~Figure 5C shows HDL/LDL samples corresponding to 2 μg protein/lane (CEL top panel) or 20 μg/lane (apoB bottom panel). CEL is abundantly present in the HDL/LDL fraction of human serum in a pattern that follows that of apoB (bottom panel). The positive control lane was loaded with 1 ng purified CEL protein.

At page 14 of the specification, please replace the paragraph at lines 10-22 with the following:

Isolation and analysis of RNA. Total RNA was isolated from monocytes and macrophages using the RNeasy-kit (Qiagen). 0.5 μg of each RNA sample was reverse transcribed in a total volume of 20 μl, using the SuperScript™. First-strand synthesis for RT-PCR (Invitrogen Life Technologies) and used in subsequent PCR-reactions. The PCR reactions were performed using the HotMaster™. Taq polymerase (Eppendorf) with the following primers used for amplification of CEL 5'-agcacctacggggatgaaga-3' (SEQ ID NO:1) and 5'-gggctcggggatcagtaacct-3' (SEQ ID NO:2) and for house-keeping gene GAPDH 5'-ccacccatggcaaattccatggca-3' (SEQ ID NO:3) and 5'-tctagacggcaggtcaggtccacc-3' (SEQ ID NO:4). Amplification of cDNA with the CEL-primers will yield a fragment of 579 bp while amplification of genomic DNA will yield a fragment of 2443 bp. Amplification of cDNA with GAPDH-primers will yield a fragment of 597 bp and while amplification of genomic DNA will yield a fragment of 1090 bp. For each PCR reaction 6 μl of the reverse-transcribed RNA was added and the following cycling parameters were used; initial denaturation at 96° C for 2 min followed by 30 cycles of 94° C for 30s, 59° C for 45s and 65° C for 2 min.